SEQUENCE LISTING

<110> SHINTANI et al.

<120> MEDICINAL USE OF MIP-3a INHIBITOR AND METHOD OF SCREENING BRAIN/NERVE CELL PROTECTIVE AGENT

<130> 20039.0001USWO

<140> 10/547,532
<141> 2005-08-31

<150> PCT/JP2004/002774
<151> 2004-03-04

<150> JP 2003-056885
<151> 2003-03-04

<150> JP 2003-106247
<151> 2003-04-10

<160> 21

<170> PatentIn version 3.1

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Met Cys Cys Thr Lys Ser Leu Leu Leu Ala Ala Leu Met Ser Val Leu
    -25                 -20                 -15
cta ctc cac ctc tgc ggc gaa tca gaa gca gca agc aac ttt gac tgc       96
Leu Leu His Leu Cys Gly Glu Ser Glu Ala Ala Ser Asn Phe Asp Cys
-10                 -5                  -1  1                   5
tgt ctt gga tac aca gac cgt att ctt cat cct aaa ttt att gtg ggc      144
Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly
            10                  15                  20
ttc aca cgg cag ctg gcc aat gaa ggc tgt gac atc aat gct atc atc      192
Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile
        25                  30                  35
ttt cac aca aag aaa aag ttg tct gtg tgc gca aat cca aaa cag act      240
Phe His Thr Lys Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr
    40                  45                  50
tgg gtg aaa tat att gtg cgt ctc ctc agt aaa aaa gtc aag aac atg      288
Trp Val Lys Tyr Ile Val Arg Leu Leu Ser Lys Lys Val Lys Asn Met
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<212> PRT
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Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly
10 15 20
Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile
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Phe His Thr Lys Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr
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Trp Val Lys Tyr Ile Val Arg Leu Leu Ser Lys Lys Val Lys Asn Met
55 60 65 70

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gct tac ctc tgc agc cag tca gaa gca gca agc aac ttt gac tgc tgc 96
Ala Tyr Leu Cys Ser Gln Ser Glu Ala Ala Ser Asn Phe Asp Cys Cys
-5 -1 1 5
ctc acg tac aca aag aac gtg tat cat cat gcg aga aat ttt gtg ggt 144
Leu Thr Tyr Thr Lys Asn Val Tyr His His Ala Arg Asn Phe Val Gly
10 15 20
ttc aca aca cag atg gcc gac gaa gct tgt gac att aat gct atc atc 192
Phe Thr Thr Gln Met Ala Asp Glu Ala Cys Asp Ile Asn Ala Ile Ile
25 30 35
ttt cac ctg aag tcg aaa aga tcc gtg tgc gct gac cca aag cag atc 240
Phe His Leu Lys Ser Lys Arg Ser Val Cys Ala Asp Pro Lys Gln Ile
40 45 50 55
tgg gtg aaa agg att ttg cac ctc ctc agc cta aga acc aag aag atg 288
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<213> Rattus norvegicus

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Leu Thr Tyr Thr Lys Asn Val Tyr His His Ala Arg Asn Phe Val Gly
10 15 20
Phe Thr Thr Gln Met Ala Asp Glu Ala Cys Asp Ile Asn Ala Ile Ile
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Phe His Leu Lys Ser Lys Arg Ser Val Cys Ala Asp Pro Lys Gln Ile
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Trp Val Lys Arg Ile Leu His Leu Leu Ser Leu Arg Thr Lys Lys Met
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ctg ctg gct cac ctc tgc agc cag gca gaa gca gca agc aac tac gac 96
Leu Leu Ala His Leu Cys Ser Gln Ala Glu Ala Ala Ser Asn Tyr Asp
-10 -5 -1 1 5
tgt tgc ctc tcg tac ata cag acg cct ctt cct tcc aga gct att gtg 144
Cys Cys Leu Ser Tyr Ile Gln Thr Pro Leu Pro Ser Arg Ala Ile Val
10 15 20
ggt ttc aca aga cag atg gcc gat gaa gct tgt gac att aat gct atc 192
Gly Phe Thr Arg Gln Met Ala Asp Glu Ala Cys Asp Ile Asn Ala Ile
25 30 35
atc ttt cac acg aag aaa aga aaa tct gtg tgc gct gat cca aag cag 240
Ile Phe His Thr Lys Lys Arg Lys Ser Val Cys Ala Asp Pro Lys Gln
40 45 50
aac tgg gtg aaa agg gct gtg aac ctc ctc agc cta aga gtc aag aag 288
Asn Trp Val Lys Arg Ala Val Asn Leu Leu Ser Leu Arg Val Lys Lys
55 60 65
atg 291
Met 70

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<400> 6

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Leu Leu Ala His Leu Cys Ser Gln Ala Glu Ala Ala Ser Asn Tyr Asp
    -10                 -5                  -1  1               5
Cys Cys Leu Ser Tyr Ile Gln Thr Pro Leu Pro Ser Arg Ala Ile Val
                10                  15                  20
Gly Phe Thr Arg Gln Met Ala Asp Glu Ala Cys Asp Ile Asn Ala Ile
            25                  30                  35
Ile Phe His Thr Lys Lys Arg Lys Ser Val Cys Ala Asp Pro Lys Gln
        40                  45                  50
Asn Trp Val Lys Arg Ala Val Asn Leu Leu Ser Leu Arg Val Lys Lys
    55                  60                  65
Met
70
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1               5                   10                  15
gat tat ttt gtg tca gtc aat act tca tat tac tca gtt gat tct gag        96
Asp Tyr Phe Val Ser Val Asn Thr Ser Tyr Tyr Ser Val Asp Ser Glu
            20                  25                  30
atg tta ctg tgc tcc ttg cag gag gtc agg cag ttc tcc agg cta ttt       144
Met Leu Leu Cys Ser Leu Gln Glu Val Arg Gln Phe Ser Arg Leu Phe
        35                  40                  45
gta ccg att gcc tac tcc ttg atc tgt gtc ttt ggc ctc ctg ggg aat       192
Val Pro Ile Ala Tyr Ser Leu Ile Cys Val Phe Gly Leu Leu Gly Asn
    50                  55                  60
att ctg gtg gtg atc acc ttt gct ttt tat aag aag gcc agg tct atg       240
Ile Leu Val Val Ile Thr Phe Ala Phe Tyr Lys Lys Ala Arg Ser Met
65                  70                  75                  80
aca gac gtc tat ctc ttg aac atg gcc att gca gac atc ctc ttt gtt       288
Thr Asp Val Tyr Leu Leu Asn Met Ala Ile Ala Asp Ile Leu Phe Val
                85                  90                  95
ctt act ctc cca ttc tgg gca gtg agt cat gcc act ggt gcg tgg gtt       336
Leu Thr Leu Pro Phe Trp Ala Val Ser His Ala Thr Gly Ala Trp Val
            100                 105                 110
ttc agc aat gcc acg tgc aag ttg cta aaa ggc atc tat gcc atc aac       384
Phe Ser Asn Ala Thr Cys Lys Leu Leu Lys Gly Ile Tyr Ala Ile Asn
        115                 120                 125
ttt aac tgc ggg atg ctg ctc ctg act tgc att agc atg gac cgg tac       432
Phe Asn Cys Gly Met Leu Leu Leu Thr Cys Ile Ser Met Asp Arg Tyr
    130                 135                 140
atc gcc att gta cag gcg act aag tca ttc cgg ctc cga tcc aga aca       480
Ile Ala Ile Val Gln Ala Thr Lys Ser Phe Arg Leu Arg Ser Arg Thr
145                 150                 155                 160
cta ccg cgc agc aaa atc atc tgc ctt gtt gtg tgg ggg ctg tca gtc       528
Leu Pro Arg Ser Lys Ile Ile Cys Leu Val Val Trp Gly Leu Ser Val
                165                 170                 175
atc atc tcc agc tca act ttt gtc ttc aac caa aaa tac aac acc caa       576
Ile Ile Ser Ser Ser Thr Phe Val Phe Asn Gln Lys Tyr Asn Thr Gln
            180                 185                 190
ggc agc gat gtc tgt gaa ccc aag tac cag act gtc tcg gag ccc atc       624
Gly Ser Asp Val Cys Glu Pro Lys Tyr Gln Thr Val Ser Glu Pro Ile
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        195                 200                 205
agg tgg aag ctg ctg atg ttg ggg ctt gag cta ctc ttt ggt ttc ttt      672
Arg Trp Lys Leu Leu Met Leu Gly Leu Glu Leu Leu Phe Gly Phe Phe
    210                 215                 220
atc cct ttg atg ttc atg ata ttt tgt tac acg ttc att gtc aaa acc      720
Ile Pro Leu Met Phe Met Ile Phe Cys Tyr Thr Phe Ile Val Lys Thr
225                 230                 235                 240
ttg gtg caa gct cag aat tct aaa agg cac aaa gcc atc cgt gta atc      768
Leu Val Gln Ala Gln Asn Ser Lys Arg His Lys Ala Ile Arg Val Ile
                245                 250                 255
ata gct gtg gtg ctt gtg ttt ctg gct tgt cag att cct cat aac atg      816
Ile Ala Val Val Leu Val Phe Leu Ala Cys Gln Ile Pro His Asn Met
            260                 265                 270
gtc ctg ctt gtg acg gct gca aat ttg ggt aaa atg aac cga tcc tgc      864
Val Leu Leu Val Thr Ala Ala Asn Leu Gly Lys Met Asn Arg Ser Cys
        275                 280                 285
cag agc gaa aag cta att ggc tat acg aaa act gtc aca gaa gtc ctg      912
Gln Ser Glu Lys Leu Ile Gly Tyr Thr Lys Thr Val Thr Glu Val Leu
    290                 295                 300
gct ttc ctg cac tgc tgc ctg aac cct gtg ctc tac gct ttt att ggg      960
Ala Phe Leu His Cys Cys Leu Asn Pro Val Leu Tyr Ala Phe Ile Gly
305                 310                 315                 320
cag aag ttc aga aac tac ttt ctg aag atc ttg aag gac ctg tgg tgt     1008
Gln Lys Phe Arg Asn Tyr Phe Leu Lys Ile Leu Lys Asp Leu Trp Cys
                325                 330                 335
gtg aga agg aag tac aag tcc tca ggc ttc tcc tgt gcc ggg agg tac     1056
Val Arg Arg Lys Tyr Lys Ser Ser Gly Phe Ser Cys Ala Gly Arg Tyr
            340                 345                 350
tca gaa aac att tct cgg cag acc agt gag acc gca gat aac gac aat     1104
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        355                 360                 365
gcg tcg tcc ttc act atg                                            1122
Ala Ser Ser Phe Thr Met                                                370
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<213> Homo sapiens

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            20                  25                  30
Met Leu Leu Cys Ser Leu Gln Glu Val Arg Gln Phe Ser Arg Leu Phe
        35                  40                  45
Val Pro Ile Ala Tyr Ser Leu Ile Cys Val Phe Gly Leu Leu Gly Asn
    50                  55                  60
Ile Leu Val Val Ile Thr Phe Ala Phe Tyr Lys Lys Ala Arg Ser Met
65                  70                  75                  80
Thr Asp Val Tyr Leu Leu Asn Met Ala Ile Ala Asp Ile Leu Phe Val
                85                  90                  95
Leu Thr Leu Pro Phe Trp Ala Val Ser His Ala Thr Gly Ala Trp Val
            100                 105                 110
Phe Ser Asn Ala Thr Cys Lys Leu Leu Lys Gly Ile Tyr Ala Ile Asn
        115                 120                 125
Phe Asn Cys Gly Met Leu Leu Leu Thr Cys Ile Ser Met Asp Arg Tyr
    130                 135                 140
Ile Ala Ile Val Gln Ala Thr Lys Ser Phe Arg Leu Arg Ser Arg Thr
145                 150                 155                 160
Leu Pro Arg Ser Lys Ile Ile Cys Leu Val Val Trp Gly Leu Ser Val
                165                 170                 175
Ile Ile Ser Ser Ser Thr Phe Val Phe Asn Gln Lys Tyr Asn Thr Gln
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            180                 185                 190
Gly Ser Asp Val Cys Glu Pro Lys Tyr Gln Thr Val Ser Glu Pro Ile
        195                 200                 205
Arg Trp Lys Leu Leu Met Leu Gly Leu Glu Leu Leu Phe Gly Phe Phe
    210                 215                 220
Ile Pro Leu Met Phe Met Ile Phe Cys Tyr Thr Phe Ile Val Lys Thr
225                 230                 235                 240
Leu Val Gln Ala Gln Asn Ser Lys Arg His Lys Ala Ile Arg Val Ile
                245                 250                 255
Ile Ala Val Val Leu Val Phe Leu Ala Cys Gln Ile Pro His Asn Met
            260                 265                 270
Val Leu Leu Val Thr Ala Ala Asn Leu Gly Lys Met Asn Arg Ser Cys
        275                 280                 285
Gln Ser Glu Lys Leu Ile Gly Tyr Thr Lys Thr Val Thr Glu Val Leu
    290                 295                 300
Ala Phe Leu His Cys Cys Leu Asn Pro Val Leu Tyr Ala Phe Ile Gly
305                 310                 315                 320
Gln Lys Phe Arg Asn Tyr Phe Leu Lys Ile Leu Lys Asp Leu Trp Cys
                325                 330                 335
Val Arg Arg Lys Tyr Lys Ser Ser Gly Phe Ser Cys Ala Gly Arg Tyr
            340                 345                 350
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        355                 360                 365
Ala Ser Ser Phe Thr Met
    370
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<222> (1)..(1101)
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1               5                   10                  15
gag tat tat tct att cct cca gac cat ggg cca tgc tcc cta gaa gag       96
Glu Tyr Tyr Ser Ile Pro Pro Asp His Gly Pro Cys Ser Leu Glu Glu
            20                  25                  30
gtc aga aac ttc acc aag gta ttt gtg cca att gcc tac tcc tta ata      144
Val Arg Asn Phe Thr Lys Val Phe Val Pro Ile Ala Tyr Ser Leu Ile
        35                  40                  45
tgt gtc ttt ggc ctc ctg ggc aac att atg gtg gtg atg acc ttt gcc      192
Cys Val Phe Gly Leu Leu Gly Asn Ile Met Val Val Met Thr Phe Ala
    50                  55                  60
ttc tac aag aaa gcc aga tcc atg act gac gtc tac ctg ttg aac atg      240
Phe Tyr Lys Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met
65                  70                  75                  80
gcc atc aca gac ata ctc ttt gtc ctc acc cta ccg ttc tgg gca gtt      288
Ala Ile Thr Asp Ile Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val
                85                  90                  95
act cat gcc acc aac act tgg gtt ttc agc gat gca ctg tgt aaa ctg      336
Thr His Ala Thr Asn Thr Trp Val Phe Ser Asp Ala Leu Cys Lys Leu
            100                 105                 110
atg aaa ggc aca tat gcg gtc aac ttt aac tgt ggg atg ctg ctc ctg      384
Met Lys Gly Thr Tyr Ala Val Asn Phe Asn Cys Gly Met Leu Leu Leu
        115                 120                 125
gcc tgt atc agc atg gac cgg tac att gcc atc gtc cag gca acc aaa      432
Ala Cys Ile Ser Met Asp Arg Tyr Ile Ala Ile Val Gln Ala Thr Lys
    130                 135                 140
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tct ttc cgg gta cgc tcc aga aca ctg acg cac agt aag gtc atc tgt      480
Ser Phe Arg Val Arg Ser Arg Thr Leu Thr His Ser Lys Val Ile Cys
145                 150                 155                 160
gtg gca gtg tgg ttc atc tcc atc atc atc tca agc cct aca ttt atc      528
Val Ala Val Trp Phe Ile Ser Ile Ile Ile Ser Ser Pro Thr Phe Ile
                165                 170                 175
ttc aac aag aaa tac gag ctg cag gat cgt gat gtc tgt gag cca cgg      576
Phe Asn Lys Lys Tyr Glu Leu Gln Asp Arg Asp Val Cys Glu Pro Arg
            180                 185                 190
tac agg tct gtc tca gag ccc atc acg tgg aag ctg ctg ggt atg gga      624
Tyr Arg Ser Val Ser Glu Pro Ile Thr Trp Lys Leu Leu Gly Met Gly
        195                 200                 205
ctg gag ctg ttc ttt ggg ttc ttc acc cct ttg ctg ttt atg gtg ttc      672
Leu Glu Leu Phe Phe Gly Phe Phe Thr Pro Leu Leu Phe Met Val Phe
    210                 215                 220
tgc tat ctg ttc att atc aag acc ttg gtg cag gcc cag aac tcc aag      720
Cys Tyr Leu Phe Ile Ile Lys Thr Leu Val Gln Ala Gln Asn Ser Lys
225                 230                 235                 240
agg cac aga gcc atc cga gtc gtg atc gct gtg gtt ctc gtg ttc ctg      768
Arg His Arg Ala Ile Arg Val Val Ile Ala Val Val Leu Val Phe Leu
                245                 250                 255
gct tgt cag atc cct cac aac atg gtc ctc ctc gtg act gcg gtc aac      816
Ala Cys Gln Ile Pro His Asn Met Val Leu Leu Val Thr Ala Val Asn
            260                 265                 270
acg ggc aaa gtg ggc cgg agc tgc agc acc gag aaa gtc ctc gcc tac      864
Thr Gly Lys Val Gly Arg Ser Cys Ser Thr Glu Lys Val Leu Ala Tyr
        275                 280                 285
acc agg aac gtg gcc gag gtc ctg gct ttc ctg cat tgc tgc ctc aac      912
Thr Arg Asn Val Ala Glu Val Leu Ala Phe Leu His Cys Cys Leu Asn
    290                 295                 300
ccc gtg ttg tat gcg ttt att gga cag aaa ttc aga aac tac ttc atg      960
Pro Val Leu Tyr Ala Phe Ile Gly Gln Lys Phe Arg Asn Tyr Phe Met
305                 310                 315                 320
aag atc atg aag gat gtg tgg tgt atg aga agg aag aat aag atg cct     1008
Lys Ile Met Lys Asp Val Trp Cys Met Arg Arg Lys Asn Lys Met Pro
                325                 330                 335
ggc ttc ctc tgt gcc cgg gtt tac tcg gaa agc tac atc tcc agg cag     1056
Gly Phe Leu Cys Ala Arg Val Tyr Ser Glu Ser Tyr Ile Ser Arg Gln
            340                 345                 350
acc agt gag acc gtc gaa aat gat aat gca tcg tcc ttt acc atg         1101
Thr Ser Glu Thr Val Glu Asn Asp Asn Ala Ser Ser Phe Thr Met
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            20                  25                  30
Val Arg Asn Phe Thr Lys Val Phe Val Pro Ile Ala Tyr Ser Leu Ile
        35                  40                  45
Cys Val Phe Gly Leu Leu Gly Asn Ile Met Val Val Met Thr Phe Ala
    50                  55                  60
Phe Tyr Lys Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met
65                  70                  75                  80
Ala Ile Thr Asp Ile Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val
                85                  90                  95
Thr His Ala Thr Asn Thr Trp Val Phe Ser Asp Ala Leu Cys Lys Leu
            100                 105                 110
Met Lys Gly Thr Tyr Ala Val Asn Phe Asn Cys Gly Met Leu Leu Leu
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        115                 120                 125
Ala Cys Ile Ser Met Asp Arg Tyr Ile Ala Ile Val Gln Ala Thr Lys
    130                 135                 140
Ser Phe Arg Val Arg Ser Arg Thr Leu Thr His Ser Lys Val Ile Cys
145                 150                 155                 160
Val Ala Val Trp Phe Ile Ser Ile Ile Ile Ser Ser Pro Thr Phe Ile
                165                 170                 175
Phe Asn Lys Lys Tyr Glu Leu Gln Asp Arg Asp Val Cys Glu Pro Arg
            180                 185                 190
Tyr Arg Ser Val Ser Glu Pro Ile Thr Trp Lys Leu Leu Gly Met Gly
        195                 200                 205
Leu Glu Leu Phe Phe Gly Phe Phe Thr Pro Leu Leu Phe Met Val Phe
    210                 215                 220
Cys Tyr Leu Phe Ile Ile Lys Thr Leu Val Gln Ala Gln Asn Ser Lys
225                 230                 235                 240
Arg His Arg Ala Ile Arg Val Val Ile Ala Val Val Leu Val Phe Leu
                245                 250                 255
Ala Cys Gln Ile Pro His Asn Met Val Leu Leu Val Thr Ala Val Asn
            260                 265                 270
Thr Gly Lys Val Gly Arg Ser Cys Ser Thr Glu Lys Val Leu Ala Tyr
        275                 280                 285
Thr Arg Asn Val Ala Glu Val Leu Ala Phe Leu His Cys Cys Leu Asn
    290                 295                 300
Pro Val Leu Tyr Ala Phe Ile Gly Gln Lys Phe Arg Asn Tyr Phe Met
305                 310                 315                 320
Lys Ile Met Lys Asp Val Trp Cys Met Arg Arg Lys Asn Lys Met Pro
                325                 330                 335
Gly Phe Leu Cys Ala Arg Val Tyr Ser Glu Ser Tyr Ile Ser Arg Gln
            340                 345                 350
Thr Ser Glu Thr Val Glu Asn Asp Asn Ala Ser Ser Phe Thr Met
        355                 360                 365
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<210> 11
<211> 20
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Oligonucleotide designed to act as primer for amplifying fragment of rat MIP-3.alpha. gene transcript.

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<210> 12
<211> 21
<212> DNA
<213> Artificial

<220>
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<223> Oligonucleotide designed to act as primer for amplifying fragment of rat MIP-3.alpha. gene transcript.

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<210> 13
<211> 1502
<212> DNA
<213> Rattus norvegicus (kidney)

<220>

<221> CDS
<222> (343)..(1443)
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ccacctgcag tttgaagtca tcactttcaa tccccctgtg actagggcca gggtcttcac 180
acctgcgaga ggaagcaaag atctaagcaa tctgaatttt aagagagaaa ctgcagctgt 240
cggtttgtgg gccggaacat tattggactg gagcctggac aagcactaag gcgggggtac 300
ctggccagcc cacttcggag ctcagcgttt ccttgggaaa cg atg aat ttc acc 354
Met Asn Phe Thr
1

gag gcc aac tac gga atg gaa gat tat act ggc tca gat tac tct atg 402
Glu Ala Asn Tyr Gly Met Glu Asp Tyr Thr Gly Ser Asp Tyr Ser Met
5 10 15 20
ttt cca gag acc gag cca tgc tct ctg caa gag gtc aga gac ttc acc 450
Phe Pro Glu Thr Glu Pro Cys Ser Leu Gln Glu Val Arg Asp Phe Thr
25 30 35
aag gtg ttc gtg cca atc gcc tac tcc tta atc tgt gtc ttt ggc ctc 498
Lys Val Phe Val Pro Ile Ala Tyr Ser Leu Ile Cys Val Phe Gly Leu
40 45 50
ctt ggc aat att atg gtg gtg ata acc ttt gcc ttc tac aag aaa gcc 546
Leu Gly Asn Ile Met Val Val Ile Thr Phe Ala Phe Tyr Lys Lys Ala
55 60 65
agg tcc atg act gac gtc tac cta ttg aac atg gcc atc aca gac ata 594
Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met Ala Ile Thr Asp Ile
70 75 80
ctc ttt gtc ctc acc cta cca ttc tgg gca gtt act cat gcc act gac 642
Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val Thr His Ala Thr Asp
85 90 95 100
act tgg atc ttt ggc aac acg atg tgt aaa ctg atg aaa ggc acg tat 690
Thr Trp Ile Phe Gly Asn Thr Met Cys Lys Leu Met Lys Gly Thr Tyr
105 110 115
gcg gtc aac ttt aac tgt ggg atg ctg ctc ctg gcc tgt atc agc atg 738
Ala Val Asn Phe Asn Cys Gly Met Leu Leu Leu Ala Cys Ile Ser Met
120 125 130
gac cgg tac att gcc atc gtc cag gcg acc aaa tct ttc cgg gta cgc 786
Asp Arg Tyr Ile Ala Ile Val Gln Ala Thr Lys Ser Phe Arg Val Arg
135 140 145
tcc aga aca ctg acg cac agt aag gtc atc tgt ctg acg gtg tgg ttc 834
Ser Arg Thr Leu Thr His Ser Lys Val Ile Cys Leu Thr Val Trp Phe
150 155 160
gtt tcc atc atc atc tca agc ccc aca ttc ttc ttc aac aag caa tac 882
Val Ser Ile Ile Ile Ser Ser Pro Thr Phe Phe Phe Asn Lys Gln Tyr
165 170 175 180
aag ctg cag ggc cgt gat gtc tgc gag cct cag tac aag ctc gtc tcg 930
Lys Leu Gln Gly Arg Asp Val Cys Glu Pro Gln Tyr Lys Leu Val Ser
185 190 195
gag ccc atc acg tgg aaa ctg ctg ggc atg gga ctc gag ctg ctc ttt 978
Glu Pro Ile Thr Trp Lys Leu Leu Gly Met Gly Leu Glu Leu Leu Phe
200 205 210
ggc ttc ttc atc cct ttg ctg ttt atg gtg ttc tgt tac ctg ttc atc 1026
Gly Phe Phe Ile Pro Leu Leu Phe Met Val Phe Cys Tyr Leu Phe Ile
215 220 225
atc aag acc ttg gtg cag gcc cag aat tcc aag agg cac aga gcc atc 1074
Ile Lys Thr Leu Val Gln Ala Gln Asn Ser Lys Arg His Arg Ala Ile
230 235 240
cga gtc gtg att gct gtg gtt ctc gtg ttc ctg gct tgt cag atc cct 1122
Arg Val Val Ile Ala Val Val Leu Val Phe Leu Ala Cys Gln Ile Pro
245 250 255 260
cac aac atg gtc ctc ctc gtg act gca gcc aac acg ggc aaa atg ggc 1170
His Asn Met Val Leu Leu Val Thr Ala Ala Asn Thr Gly Lys Met Gly
265 270 275

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cgc agc tgc agc gcc gag aaa gcc ctc gcc tac gcc agg aat gtg gct     1218
Arg Ser Cys Ser Ala Glu Lys Ala Leu Ala Tyr Ala Arg Asn Val Ala
            280                 285                 290
gag gtc ctg gct ttc ctg cac tgc tgt ctc aac ccc gtg ttg tat gcc     1266
Glu Val Leu Ala Phe Leu His Cys Cys Leu Asn Pro Val Leu Tyr Ala
        295                 300                 305
ttc att gga cag aaa ttc aga agc tac ttc atg aag atc atg aag gat     1314
Phe Ile Gly Gln Lys Phe Arg Ser Tyr Phe Met Lys Ile Met Lys Asp
    310                 315                 320
gtg tgg tgt atg agg agg aag agc aag gtg cct acc ttc ttc tgt gcc     1362
Val Trp Cys Met Arg Arg Lys Ser Lys Val Pro Thr Phe Phe Cys Ala
325                 330                 335                 340
cgg gtt tac tca gaa agc tac atc tcc agg cag acc agt gag act gta     1410
Arg Val Tyr Ser Glu Ser Tyr Ile Ser Arg Gln Thr Ser Glu Thr Val
                345                 350                 355
gaa aat gac aac gca tcg tcc ttt acc atg taa cacgagagca caaagcagca   1463
Glu Asn Asp Asn Ala Ser Ser Phe Thr Met
            360                 365
tgccccgaaa gcctttgtga aacttgctat tacatgtga                          1502
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<210> 14
<211> 366
<212> PRT
<213> Rattus norvegicus

<400> 14

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Met Asn Phe Thr Glu Ala Asn Tyr Gly Met Glu Asp Tyr Thr Gly Ser
1               5                   10                  15
Asp Tyr Ser Met Phe Pro Glu Thr Glu Pro Cys Ser Leu Gln Glu Val
            20                  25                  30
Arg Asp Phe Thr Lys Val Phe Val Pro Ile Ala Tyr Ser Leu Ile Cys
        35                  40                  45
Val Phe Gly Leu Leu Gly Asn Ile Met Val Val Ile Thr Phe Ala Phe
    50                  55                  60
Tyr Lys Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met Ala
65                  70                  75                  80
Ile Thr Asp Ile Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val Thr
                85                  90                  95
His Ala Thr Asp Thr Trp Ile Phe Gly Asn Thr Met Cys Lys Leu Met
            100                 105                 110
Lys Gly Thr Tyr Ala Val Asn Phe Asn Cys Gly Met Leu Leu Leu Ala
        115                 120                 125
Cys Ile Ser Met Asp Arg Tyr Ile Ala Ile Val Gln Ala Thr Lys Ser
    130                 135                 140
Phe Arg Val Arg Ser Arg Thr Leu Thr His Ser Lys Val Ile Cys Leu
145                 150                 155                 160
Thr Val Trp Phe Val Ser Ile Ile Ile Ser Ser Pro Thr Phe Phe Phe
                165                 170                 175
Asn Lys Gln Tyr Lys Leu Gln Gly Arg Asp Val Cys Glu Pro Gln Tyr
            180                 185                 190
Lys Leu Val Ser Glu Pro Ile Thr Trp Lys Leu Leu Gly Met Gly Leu
        195                 200                 205
Glu Leu Leu Phe Gly Phe Phe Ile Pro Leu Leu Phe Met Val Phe Cys
    210                 215                 220
Tyr Leu Phe Ile Ile Lys Thr Leu Val Gln Ala Gln Asn Ser Lys Arg
225                 230                 235                 240
His Arg Ala Ile Arg Val Val Ile Ala Val Val Leu Val Phe Leu Ala
                245                 250                 255
Cys Gln Ile Pro His Asn Met Val Leu Leu Val Thr Ala Ala Asn Thr
            260                 265                 270
Gly Lys Met Gly Arg Ser Cys Ser Ala Glu Lys Ala Leu Ala Tyr Ala
        275                 280                 285
Arg Asn Val Ala Glu Val Leu Ala Phe Leu His Cys Cys Leu Asn Pro
    290                 295                 300
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Val Leu Tyr Ala Phe Ile Gly Gln Lys Phe Arg Ser Tyr Phe Met Lys
305                 310                 315                 320
Ile Met Lys Asp Val Trp Cys Met Arg Arg Lys Ser Lys Val Pro Thr
                325                 330                 335
Phe Phe Cys Ala Arg Val Tyr Ser Glu Ser Tyr Ile Ser Arg Gln Thr
            340                 345                 350
Ser Glu Thr Val Glu Asn Asp Asn Ala Ser Ser Phe Thr Met
        355                 360                 365
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<210> 15
<211> 1309
<212> DNA
<213> Rattus norvegicus (liver)

<220>
<221> CDS
<222> (150)..(1250)
<223>

<400> 15

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gcatctcact acccgtctct caatgagcac cgctggttgt gcctgtcaac agaatagtcc     60
tctcacactt aggactggag cctggacaag cactaaggcg ggggtacctg gccagcccac    120
ttcggagctc agcgtttcct tgggaaacg atg aat ttc acc gag gcc aac tac       173
                               Met Asn Phe Thr Glu Ala Asn Tyr
                               1               5
gga atg gaa gat tat act ggc tca gat tac tct atg ttt cca gag acc       221
Gly Met Glu Asp Tyr Thr Gly Ser Asp Tyr Ser Met Phe Pro Glu Thr
    10                  15                  20
gag cca tgc tct ctg caa gag gtc aga gac ttc acc aag gtg ttc gtg       269
Glu Pro Cys Ser Leu Gln Glu Val Arg Asp Phe Thr Lys Val Phe Val
25                  30                  35                  40
cca atc gcc tac tcc tta atc tgt gtc ttt ggc ctc ctt ggc aat att       317
Pro Ile Ala Tyr Ser Leu Ile Cys Val Phe Gly Leu Leu Gly Asn Ile
                45                  50                  55
atg gtg gtg ata acc ttt gcc ttc tac aag aaa gcc agg tcc atg act       365
Met Val Val Ile Thr Phe Ala Phe Tyr Lys Lys Ala Arg Ser Met Thr
            60                  65                  70
gac gtc tac cta ttg aac atg gcc atc aca gac ata ctc ttt gtc ctc       413
Asp Val Tyr Leu Leu Asn Met Ala Ile Thr Asp Ile Leu Phe Val Leu
        75                  80                  85
acc cta cca ttc tgg gca gtt act cat gcc act gac act tgg atc ttt       461
Thr Leu Pro Phe Trp Ala Val Thr His Ala Thr Asp Thr Trp Ile Phe
    90                  95                  100
ggc aac acg atg tgt aaa ctg atg aaa ggc acg tat gcg gtc aac ttt       509
Gly Asn Thr Met Cys Lys Leu Met Lys Gly Thr Tyr Ala Val Asn Phe
105                 110                 115                 120
aac tgt ggg atg ctg ctc ctg gcc tgt atc agc atg gac cgg tac att       557
Asn Cys Gly Met Leu Leu Leu Ala Cys Ile Ser Met Asp Arg Tyr Ile
                125                 130                 135
gcc atc gtc cag gcg acc aaa tct ttc cgg gta cgc tcc aga aca ctg       605
Ala Ile Val Gln Ala Thr Lys Ser Phe Arg Val Arg Ser Arg Thr Leu
            140                 145                 150
acg cac agt aag gtc atc tgt ctg acg gtg tgg ttc gtt tcc atc atc       653
Thr His Ser Lys Val Ile Cys Leu Thr Val Trp Phe Val Ser Ile Ile
        155                 160                 165
atc tca agc ccc aca ttc ttc ttc aac aag caa tac aag ctg cag ggc       701
Ile Ser Ser Pro Thr Phe Phe Phe Asn Lys Gln Tyr Lys Leu Gln Gly
    170                 175                 180
cgt gat gtc tgc gag cct cag tac aag ctc gtc tcg gag ccc atc acg       749
Arg Asp Val Cys Glu Pro Gln Tyr Lys Leu Val Ser Glu Pro Ile Thr
185                 190                 195                 200
tgg aaa ctg ctg ggc atg gga ctc gag ctg ctc ttt ggc ttc ttc atc       797
Trp Lys Leu Leu Gly Met Gly Leu Glu Leu Leu Phe Gly Phe Phe Ile
                205                 210                 215
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cct ttg ctg ttt atg gtg ttc tgt tac ctg ttc atc atc aag acc ttg      845
Pro Leu Leu Phe Met Val Phe Cys Tyr Leu Phe Ile Ile Lys Thr Leu
            220                 225                 230
gtg cag gcc cag aat tcc aag agg cac aga gcc atc cga gtc gtg att      893
Val Gln Ala Gln Asn Ser Lys Arg His Arg Ala Ile Arg Val Val Ile
        235                 240                 245
gct gtg gtt ctc gtg ttc ctg gct tgt cag atc cct cac aac atg gtc      941
Ala Val Val Leu Val Phe Leu Ala Cys Gln Ile Pro His Asn Met Val
    250                 255                 260
ctc ctc gtg act gca gcc aac acg ggc aaa atg ggc cgc agc tgc agc      989
Leu Leu Val Thr Ala Ala Asn Thr Gly Lys Met Gly Arg Ser Cys Ser
265                 270                 275                 280
gcc gag aaa gcc ctc gcc tac gcc agg aat gtg gct gag gtc ctg gct     1037
Ala Glu Lys Ala Leu Ala Tyr Ala Arg Asn Val Ala Glu Val Leu Ala
                285                 290                 295
ttc ctg cac tgc tgt ctc aac ccc gtg ttg tat gcc ttc att gga cag     1085
Phe Leu His Cys Cys Leu Asn Pro Val Leu Tyr Ala Phe Ile Gly Gln
            300                 305                 310
aaa ttc aga agc tac ttc atg aag atc atg aag gat gtg tgg tgt atg     1133
Lys Phe Arg Ser Tyr Phe Met Lys Ile Met Lys Asp Val Trp Cys Met
        315                 320                 325
agg agg aag agc aag gtg cct acc ttc ttc tgt gcc cgg gtt tac tca     1181
Arg Arg Lys Ser Lys Val Pro Thr Phe Phe Cys Ala Arg Val Tyr Ser
    330                 335                 340
gaa agc tac atc tcc agg cag acc agt gag act gta gaa aat gac aac     1229
Glu Ser Tyr Ile Ser Arg Gln Thr Ser Glu Thr Val Glu Asn Asp Asn
345                 350                 355                 360
gca tcg tcc ttt acc atg taa cacgagagca caaagcagca tgccccgaaa        1280
Ala Ser Ser Phe Thr Met
                365
gcctttgtga aacttgctat tacatgtga                                    1309
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<210> 16
<211> 25
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide designed to act as primer for amplifying CCR6 cDNA derived from rat kidney.

<400> 16
tgtattgaag acagaacact tgtgg 25

<210> 17
<211> 28
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide designed to act as primer for amplifying CCR6 cDNA derived from rat kidney or rat liver.

<400> 17
tcacatgtaa tagcaagttt cacaaagg 28

<210> 18
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide designed to act as primer for amplifying CCR6 cDNA derived from rat liver.

<400> 18
gcatctcact acccgtctct c 21

<210> 19
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide designed to act as primer for amplifying fragment of rat CCR6 gene transcript.

<400> 19
ggacgatgcg ttgtcatttt c 21

<210> 20
<211> 22
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide designed to act as primer for amplifying fragment of rat CCR6 gene transcript.

<400> 20
ccgcagctgc agcgccgaga aa 22

<210> 21
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide designed to act as primer for amplifying fragment of rat CCR6 gene transcript.

<400> 21
gtgcccgggt ttactcagaa 20